

SEQUENCE LISTING

<110> Bayer HealthCare AG

<120> Diagnostics and Therapeutics for Diseases Associated with Mosaic Serine
Protease (MSP)

<130> BHC 03 01 007

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 2380

<212> DNA

<213> Homo sapiens

<400> 1

```

cgccccgggca gggtgagaag ccagggggcca agatggatct tctctcgac atcagctaag      60
cctggaggac tcttcccctc agagaccatg gagagggaca gccacgggaa tgcattctcca      120
gcaagaacac cttcagctgg agcatctcca gccaggcat ctccagctgg gacacctcca      180
ggccggggcat ctccagccca ggcatctcca gccaggcat ctccagctgg gacacctccg      240
ggccggggcat ctccagccca ggcatctcca gctggtacac ctccaggccg ggcatctcca      300
ggccggggcat ctccagccca ggcatctcca gccggggcat ctccggctct ggcatcactt      360
tccaggtcct catccggcag gtcattcatc gccaggctcag cctcgggtgac aacctcccca      420
accagagtgt acctgtttag agcaaaccca gtgggggctg taccatccg atcatctcct      480
gccaggtcag caccagcaac cagggccacc agggagagcc caggtagcag cctgcccagg      540
ttcacctggc gggagggcca gaagcagcta ccgctcatcg ggtgctgct cctcctcatt      600
gccctggtgg ttctgctcat catcctcttc cagttctggc agggccacac agggatcagg      660
caaaaggagc agaggagag ctgtcccaag cacgctgttc gctgtgacgg ggtggtggac      720
tgcaagctga agagtacga gctgggctgc gtgaggtttg actgggacaa gtctctgctt      780
aaaatctact ctgggtcctc ccatcagtgg ctcccatct gtagcagcaa ctggaatgac      840
tctactcag agaagacctg ccagcagctg ggtttcgaga gtgctcacg gacaaccgag      900
gttgcccaca gggattttgc caacagcttc tcaatcttga gatacaactc caccatccag      960
gaaagcctcc acaggtctga atgcccttcc cagcgggtata tctccctcca gtgttcccac     1020
tgcgactga gggccatgac cgggaggatc gtgggagggg cgctggcctc ggatagcaag     1080
tggccttggc aagtgagtct gcacttcggc accaccaca tctgtggagg cacgctcatt     1140
gacgccagct ggggtgctcac tgccgcccac tgettcttcg tgaccggga gaaggtcctg     1200
gagggctgga aggtgtacgc gggcaccagc aacctgcacc agttgcctga ggcagcctcc     1260
attgccgaga tcatcatcaa cagcaattac accgatgagg aggacgacta tgacatcgcc     1320
ctcatgccc tgtccaagcc cctgacctg tccgctcaca tccacctgc ttgcctcccc     1380
atgcatggac agacctttag cctcaatgag acctgctgga tcacaggctt tggcaagacc     1440
agggagacag atgacaagac atcccccttc ctccgggagg tgcaggtcaa tctcatcgac     1500
ttcaagaaat gcaatgacta cttggtctat gacagttacc ttaccccaag gatgatgtgt     1560
gctggggacc ttcgtggggg cagagactcc tgccagggag acagcggggg gcctcttgtc     1620

```

```

tgtgagcaga acaaccgctg gtacctggca ggtgtcacca gctggggcac aggctgtggc 1680
cagagaaaca aacctggtgt gtacaccaaa gtgacagaag ttcttccttg gatttacagc 1740
aagatggagg taagatccct gcagcaggac actgcaccca gcaggctggg aacttcctca 1800
ggtgggggacc ctggaggagc acccaggggtg taggcagagg tcccctcagc gtcccatat 1860
tcgggggggtg ttctggacag ggtcaaatgt gatgcctggg gtcaatccca gctgtctgtg 1920
tttctttccc tgcttttctt ccctcagaac agagctcagc ggggtgaaaa aggggtggacc 1980
tacaggccag gcaggcagtt gctgggcaga tgttctccca gaagtatttt tttgtgtaag 2040
gttgcaatgg actttgaaaa cgtttcagtt tctgcagagg attttgtgat agtctttgtt 2100
atcaagcatt tatgcatggg aatccgctct tcatggcctt tcccagctct gtttgtttta 2160
gtctttttga tttctttttt gttgttgttg ttgtcttttt taaaaaacac aagtgactcc 2220
attttaactc tgacaacttt cacagctgtc accagaatgc tccctgagaa ctaccattct 2280
ttccctttcc cacttaaaat atttcacag aacctcacca ctatcataaa agagtataaa 2340
gtaataaaat aataaaaagc gaaaaaaaaa aaaaaaaaaa 2380

```

<210> 2

<211> 581

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Glu Arg Asp Ser His Gly Asn Ala Ser Pro Ala Arg Thr Pro Ser
1          5          10          15
Ala Gly Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr Pro Pro Gly
          20          25          30
Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly
          35          40          45
Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr
          50          55          60
Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser
65          70          75          80
Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser
          85          90          95
Gly Arg Ser Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr
          100          105          110
Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg
          115          120          125
Ser Ser Pro Ala Arg Ser Ala Pro Ala Thr Arg Ala Thr Arg Glu Ser
          130          135          140
Pro Gly Thr Ser Leu Pro Lys Phe Thr Trp Arg Glu Gly Gln Lys Gln
145          150          155          160
Leu Pro Leu Ile Gly Cys Val Leu Leu Leu Ile Ala Leu Val Val Ser
          165          170          175
Leu Ile Ile Leu Phe Gln Phe Trp Gln Gly His Thr Gly Ile Arg His
          180          185          190
Lys Glu Gln Arg Glu Ser Cys Pro Lys His Ala Val Arg Cys Asp Gly
          195          200          205

```

Val	Val	Asp	Cys	Lys	Leu	Lys	Ser	Asp	Glu	Leu	Gly	Cys	Val	Arg	Phe	210	215	220	
Asp	Trp	Asp	Lys	Ser	Leu	Leu	Lys	Ile	Tyr	Ser	Gly	Ser	Ser	His	Gln	225	230	235	240
Trp	Leu	Pro	Ile	Cys	Ser	Ser	Asn	Trp	Asn	Asp	Ser	Tyr	Ser	Glu	Lys	245	250	255	
Thr	Cys	Arg	Gln	Leu	Gly	Phe	Glu	Ser	Ala	His	Arg	Thr	Thr	Glu	Val	260	265	270	
Ala	His	Arg	Asp	Phe	Ala	Asn	Ser	Phe	Ser	Ile	Leu	Arg	Tyr	Asn	Ser	275	280	285	
Thr	Ile	Gln	Glu	Ser	Leu	His	Arg	Ser	His	Cys	Pro	Ser	Gln	Arg	Tyr	290	295	300	
Ile	Ser	Leu	Gln	Cys	Ser	His	Cys	Gly	Leu	Arg	Ala	Met	Thr	Gly	Arg	305	310	315	320
Ile	Val	Gly	Gly	Ala	Leu	Ala	Ser	Asp	Ser	Lys	Trp	Pro	Trp	Gln	Val	325	330	335	
Ser	Leu	His	Phe	Gly	Thr	Thr	His	Ile	Cys	Gly	Gly	Thr	Leu	Ile	Asp	340	345	350	
Ala	Gln	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Phe	Phe	Val	Thr	Arg	Glu	355	360	365	
Lys	Val	Leu	Glu	Gly	Trp	Lys	Val	Tyr	Ala	Gly	Thr	Ser	Asn	Leu	His	370	375	380	
Gln	Leu	Pro	Glu	Ala	Ala	Ser	Ile	Ala	Glu	Ile	Ile	Ile	Asn	Ser	Asn	385	390	395	400
Tyr	Thr	Asp	Glu	Glu	Asp	Asp	Tyr	Asp	Ile	Ala	Leu	Met	Arg	Leu	Ser	405	410	415	
Lys	Pro	Leu	Thr	Leu	Ser	Ala	His	Ile	His	Pro	Ala	Cys	Leu	Pro	Met	420	425	430	
His	Gly	Gln	Thr	Phe	Ser	Leu	Asn	Glu	Thr	Cys	Trp	Ile	Thr	Gly	Phe	435	440	445	
Gly	Lys	Thr	Arg	Glu	Thr	Asp	Asp	Lys	Thr	Ser	Pro	Phe	Leu	Arg	Glu	450	455	460	
Val	Gln	Val	Asn	Leu	Ile	Asp	Phe	Lys	Lys	Cys	Asn	Asp	Tyr	Leu	Val	465	470	475	480
Tyr	Asp	Ser	Tyr	Leu	Thr	Pro	Arg	Met	Met	Cys	Ala	Gly	Asp	Leu	His	485	490	495	
Gly	Gly	Arg	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	500	505	510	
Glu	Gln	Asn	Asn	Arg	Trp	Tyr	Leu	Ala	Gly	Val	Thr	Ser	Trp	Gly	Thr	515	520	525	
Gly	Cys	Gly	Gln	Arg	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Thr	Glu	530	535	540	
Val	Leu	Pro	Trp	Ile	Tyr	Ser	Lys	Met	Glu	Val	Arg	Ser	Leu	Gln	Gln	545	550	555	560
Asp	Thr	Ala	Pro	Ser	Arg	Leu	Gly	Thr	Ser	Ser	Gly	Gly	Asp	Pro	Gly	565	570	575	

Gly Ala Pro Arg Val
580

<210> 3
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> forward primer

<400> 3
gcctccacag gtctgaatgc 20

<210> 4
<211> 19
<212> DNA
<213> artificial sequence

<220>
<223> reverse primer

<400> 4
cagtccgcag tgggaacac 19

<210> 5
<211> 23
<212> DNA
<213> artificial sequence

<220>
<223> probe

<400> 5
cttcccagcg gtatatctcc etc 23